Input file Fbh21620f1.seq; Output File 21620.trans
Sequence length 1909

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TACTTAGACTCAGCCGGCTTTTCCACGCTTTGCCTGACCCTGCTTTGCTCAACTGTACGTCTTGTTTCGTTTTCTGTTC

TGCGCCGTTACAGATCCAAGCTCTGAAAAACCAGAAAGTTAACTGGTAAGTTTAGTCTTTTTGTCTTTTATTTCAGGTC

CCGGATCCGGTGATCCAAATCTAAGAACTGCTCCTCAGTGAGTGTTGCCTTTACTTCTAGGCCTGTACGGAAGTGTTAC

TTCTGCTCTAAAAGCTGCGGAATTCTAATACGACTCACTATAGGGAGTCGACCCACGCGTCCGGGGTCTAGGCGCGGAT

CGGACCCAAGCAGGTCGGCGGCGGCGGCAGGAGAGCGGCCGGGCGTCAGCTCCTCGACCCCCGTGTCGGGCTAGTCCAG

                                M   A   R   P   G   M   E   R   W   R   D   R   L      13
CGAGGCGGACGGGCGGCGTGGGCCC ATG GCC AGG CCC GGC ATG GAG CGG TGG CGC GAC CGG CTG      39

 A   L   V   T   G   A   S   G   G   I   G   A   A   V   A   R   A   L   V   Q      33
GCG CTG GTG ACG GGG GCC TCG GGG GGC ATC GGC GCG GCC GTG GCC CGG GCC CTG GTC CAG      99

 Q   G   L   K   V   V   G   C   A   R   T   V   G   N   I   E   E   L   A   A      53
CAG GGA CTG AAG GTG GTG GGC TGC GCC CGC ACT GTG GGC AAC ATC GAG GAG CTG GCT GCT     159

 E   C   K   S   A   G   Y   P   G   T   L   I   P   Y   R   C   D   L   S   N      73
GAA TGT AAG AGT GCA GGC TAC CCC GGG ACT TTG ATC CCC TAC AGA TGT GAC CTA TCA AAT     219

 E   E   D   I   L   S   M   F   S   A   I   R   S   Q   H   S   G   V   D   I      93
GAA GAG GAC ATC CTC TCC ATG TTC TCA GCT ATC CGT TCT CAG CAC AGC GGT GTA GAC ATC     279

 C   I   N   N   A   G   L   A   R   P   D   T   L   L   S   G   S   T   S   G     113
TGC ATC AAC AAT GCT GGC TTG GCC CGG CCT GAC ACC CTG CTC TCA GGC AGC ACC AGT GGT     339

 W   K   D   M   F   N   V   N   V   L   A   L   S   I   C   T   R   E   A   Y     133
TGG AAG GAC ATG TTC AAT GTG AAC GTG CTG GCC CTC AGC ATC TGC ACA CGG GAA GCC TAC     399

 Q   S   M   K   E   R   N   V   D   D   G   H   I   I   N   I   N   S   M   S     153
CAG TCC ATG AAG GAG CGG AAT GTG GAC GAT GGG CAC ATC ATT AAC ATC AAT AGC ATG TCT     459

 G   H   R   V   L   P   L   S   V   T   H   F   Y   S   A   T   K   Y   A   V     173
GGC CAC CGA GTG TTA CCC CTG TCT GTG ACC CAC TTC TAT AGT GCC ACC AAG TAT GCC GTC     519

 T   A   L   T   E   G   L   R   Q   E   L   R   E   A   Q   T   H   I   R   A     193
ACT GCG CTG ACA GAG GGA CTG AGG CAA GAG CTT CGG GAG GCC CAG ACC CAC ATC CGA GCC     579

 T   C   I   S   P   G   V   V   E   T   Q   F   A   F   K   L   H   D   K   D     213
ACG TGC ATC TCT CCA GGT GTG GTG GAG ACA CAA TTC GCC TTC AAA CTC CAC GAC AAG GAC     639

 P   E   K   A   A   A   T   Y   E   Q   M   K   C   L   K   P   E   D   V   A     233
CCT GAG AAG GCA GCT GCC ACC TAT GAG CAA ATG AAG TGT CTC AAA CCC GAG GAT GTG GCC     699

 E   A   V   I   Y   V   L   S   T   P   A   H   I   Q   I   G   D   I   Q   M     253
GAG GCT GTT ATC TAC GTC CTC AGC ACT CCC GCA CAC ATC CAG ATT GGA GAC ATC CAG ATG     759

 R   P   T   E   Q   V   T   *                                                     261
AGG CCC ACG GAG CAG GTG ACC TAG                                                    783

TGACTGTGGGAGCTCCTCCTTCCCTCCCCACCCTTCATGGCTTGCCTCCTGCCTCTGGATTTTAGGTGTTGATTTCTGG

ATCACGGGATACCACTTCCTGTCCACACCCCGACCAGGGGCTAGAAAATTTGTTTGAGATTTTTATATCATCTTGTCAA

ATTGCTTCAGTTGTAAATGTGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCCTAATTGTTTTACTTGTTAACTTGTTC
```

FIGURE 1

TTGTGCCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAAATCC

CCATCTTCTTGCACCTCAACGTCTGTGGCTYANGGGCTGGGGTGGCAGAGGGAGGCCTTCACCTTATATCTGTGTTGTT

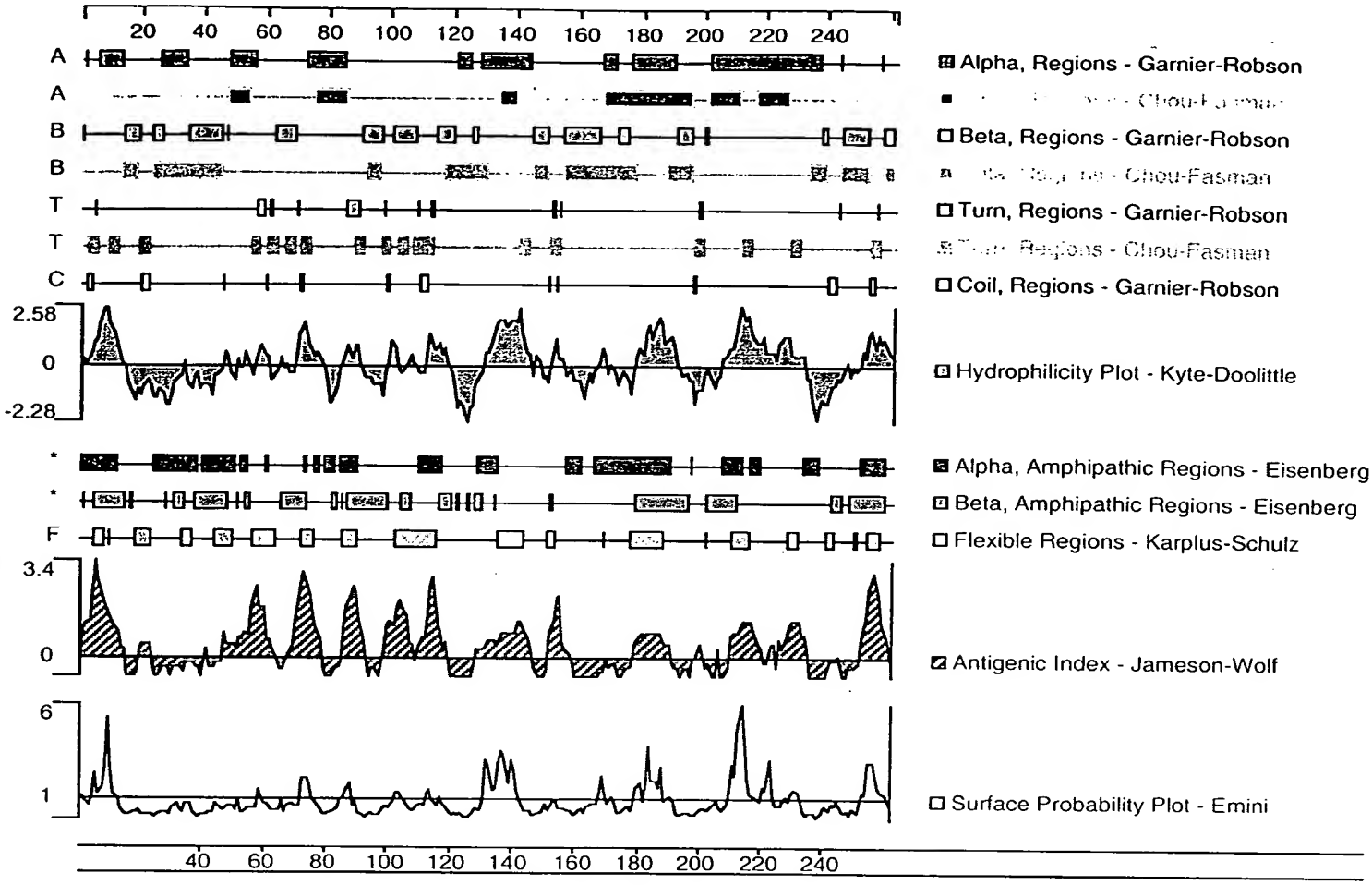
ATCCAGGGCTCCAGACTTCCTCCTCTGCCTGCCCCACTGCACCCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCCAG

CCCAGTCTTGGCTTCTTGTCCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACACCAGGGCCT

GGCCCAGTGGATTTCATGGTGATCATTAAAAAAGAAAAATCGCAACCAAAAAAAAAAAAAAAAAGGGCGGGCCGCTAGAC

TAGTYTAGAGAAAAAACCTCCCACACCTCCCCYBDAMMYTKACGCCGNACGCNANGGGGGCAATCAAGGACGCT

FIGURE 1, Page 2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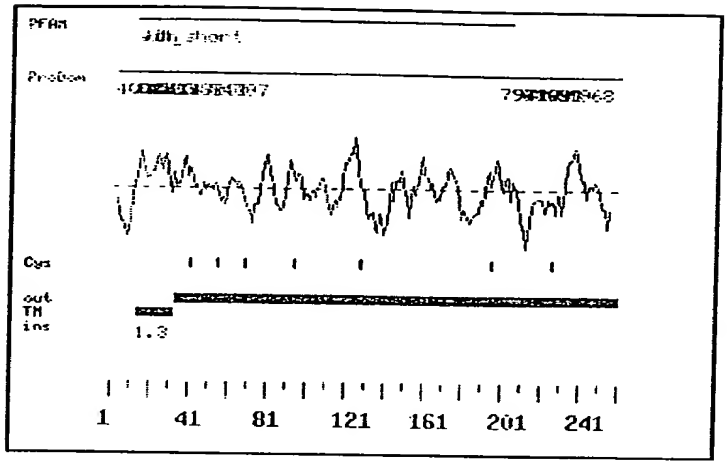
A
A
B
B
T
T
C
Alpha, Regions - Garnier-Robson
Beta, Regions - Garnier-Robson
Turn, Regions - Garnier-Robson
Coil, Regions - Garnier-Robson
2.58
0
-2.28
Hydrophilicity Plot - Kyte-Doolittle
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
F
Flexible Regions - Karplus-Schulz
3.4
0
Antigenic Index - Jameson-Wolf
6
1
Surface Probability Plot - Emini
40 60 80 100 120 140 160 180 200 220 240

FIGURE 2

Back to orfanal.cgi

Analysis of 21620 (260 aa)



Signal Peptide Predictions for 21620

Method	Predict	Score	Mat@
SignalP (eukaryote)	NO		

Note: amino-terminal 70aa used for signal peptide prediction

Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
13	32	ins-->out	1.3

FIGURE 3

Prosite Pattern Matches [redacted]21620

>PS00005|PDOC00005|PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 135 SMK 137

>PS00006|PDOC00006|CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 72 SNEE 75

Query: 89 SGVD 92

Query: 135 SMKE 138

>PS00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 18 GASGGI 23

Query: 24 GAAVAR 29

Query: 40 GCARTV 45

Query: 90 GVDICI 95

Query: 109 GSTSGW 114

Query: 199 GVVETQ 204

>PS00061|PDOC00060|ADH_SHORT Short-chain alcohol dehydrogenase family signature.

Query: 166 YSATKYAVTAL 176

FIGURE 4

ADH21620

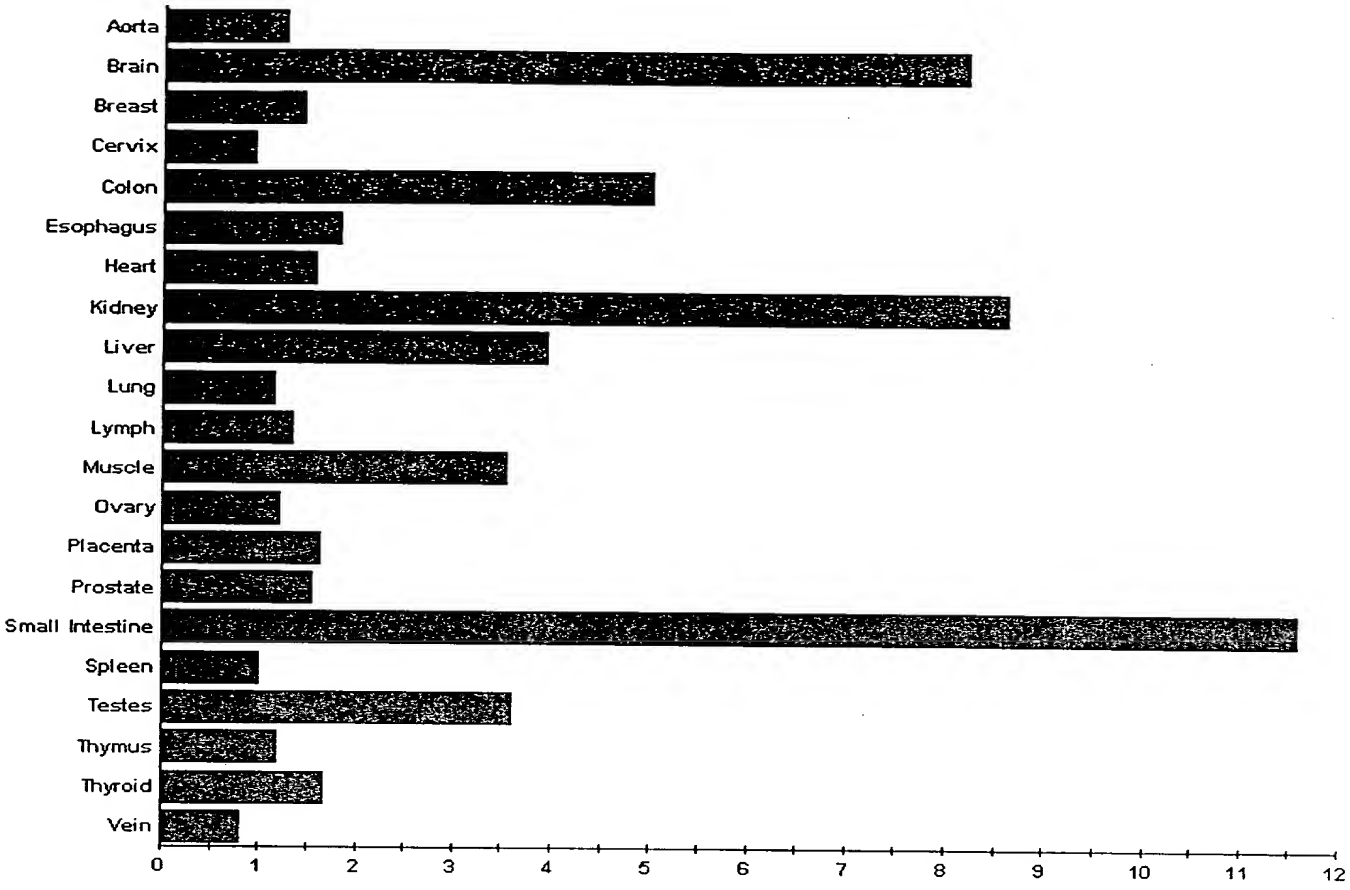


FIGURE 5

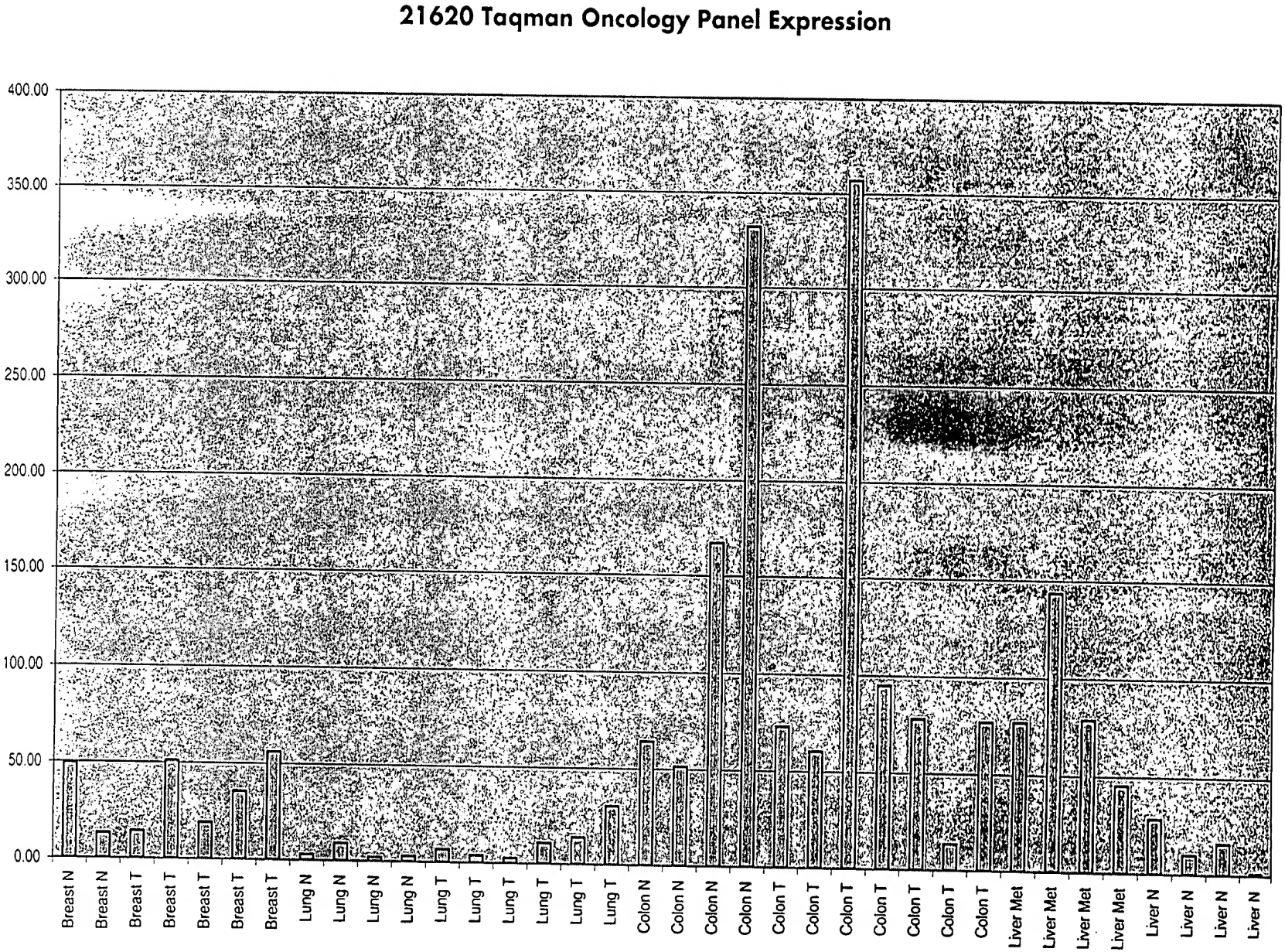


FIGURE 6

Input file Fbh33756.seq; Output File 33756.trans
Sequence length 1153

CCGCGCCCCGCCCTCGCAGCCCANNTNCGGACGCGGGCCCAGCCGCGCCTGCGCTTCCGCTCGCCTGTGGCTGCAANNA

GCGCGCTCTTCCTCGGAGCTACCCAGGCGGCTGGTGTAGCAGCAAGCTCCGCGCCGACCCCTGACGCCTGACGCCTGTC

CCCGGCCCGGCATGAGCCGCTACCTGCTGCCGCTGTCGGCGCTGGGCACGGTAGCAGGCGCTCGCCGTGCTGCTCAAGA

M E K C E A A A K D I R G 13
GGCAACATCATCCTGGCCTGCCGAGAC ATG GAG AAG TGT GAG GCG GCA GCA AAG GAC ATC CGC GGG 39

E T L N H H V N A R H L D L A S L K S I 33
GAG ACC CTC AAT CAC CAT GTC AAC GCC CGG CAC CTG GAC TTG GCT TCC CTC AAG TCT ATC 99

R E F A A K I I E E E E R V D I L I N N 53
CGA GAG TTT GCA GCA AAG ATC ATT GAA GAG GAG GAG CGA GTG GAC ATT CTA ATC AAC AAC 159

A G V M R C P H W T T E D G F E M Q F G 73
GCG GGT GTG ATG CGG TGC CCC CAC TGG ACC ACC GAG GAC GGC TTC GAG ATG CAG TTT GGC 219

V N H L G H F L L T N L L L D K L K A S 93
GTT AAC CAC CTG GGT CAC TTT CTC TTG ACA AAC TTG CTG CTG GAC AAG CTG AAA GCC TCA 279

A P S R I I N L S S L A H V A G H I D F 113
GCC CCT TCG CGG ATC ATC AAC CTC TCG TCC CTG GCC CAT GTT GCT GGG CAC ATA GAC TTT 339

D D L N W Q T R K Y N T K A A Y C Q S K 133
GAC GAC TTG AAC TGG CAG ACG AGG AAG TAT AAC ACC AAA GCC GCC TAC TGC CAG AGC AAG 399

L A I V L F T K E L S R R L Q G S G V T 153
CTC GCC ATC GTC CTC TTC ACC AAG GAG TTG AGC CGG CGG CTG CAA GGC TCT GGT GTG ACT 459

V N A L H P G V A R T E L G R H T G I H 173
GTC AAC GCC CTG CAC CCC GGC GTG GCC AGG ACA GAG CTG GGC AGA CAC ACG GGC ATC CAT 519

G S T F S S T T L G P I F W L L V K S P 193
GGC TCC ACC TTC TCC AGC ACC ACA CTC GGG CCC ATC TTC TGG CTG CTG GTC AAG AGC CCC 579

E L A A Q P S T Y L A V A E E L A D V S 213
GAG CTG GCC GCC CAG CCC AGC ACA TAC CTG GCC GTG GCG GAG GAA CTG GCG GAT GTT TCC 639

G K Y F D G L K Q K A P A P E A E D E E 233
GGA AAG TAC TTC GAT GGA CTC AAA CAG AAG GCC CCG GCC CCC GAG GCT GAG GAT GAG GAG 699

V A R R L W A E S A R L V G L E A P S V 253
GTG GCC CGG AGG CTT TGG GCT GAA AGT GCC CGC CTG GTG GGC TTA GAG GCT CCC TCT GTG 759

R E Q P L P R * 261
AGG GAG CAG CCC CTC CCC AGA TAA 783

CCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAGACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCCTGGCA

CTACCTGAGCCGGGAGACCCAGGACTG

FIGURE 7

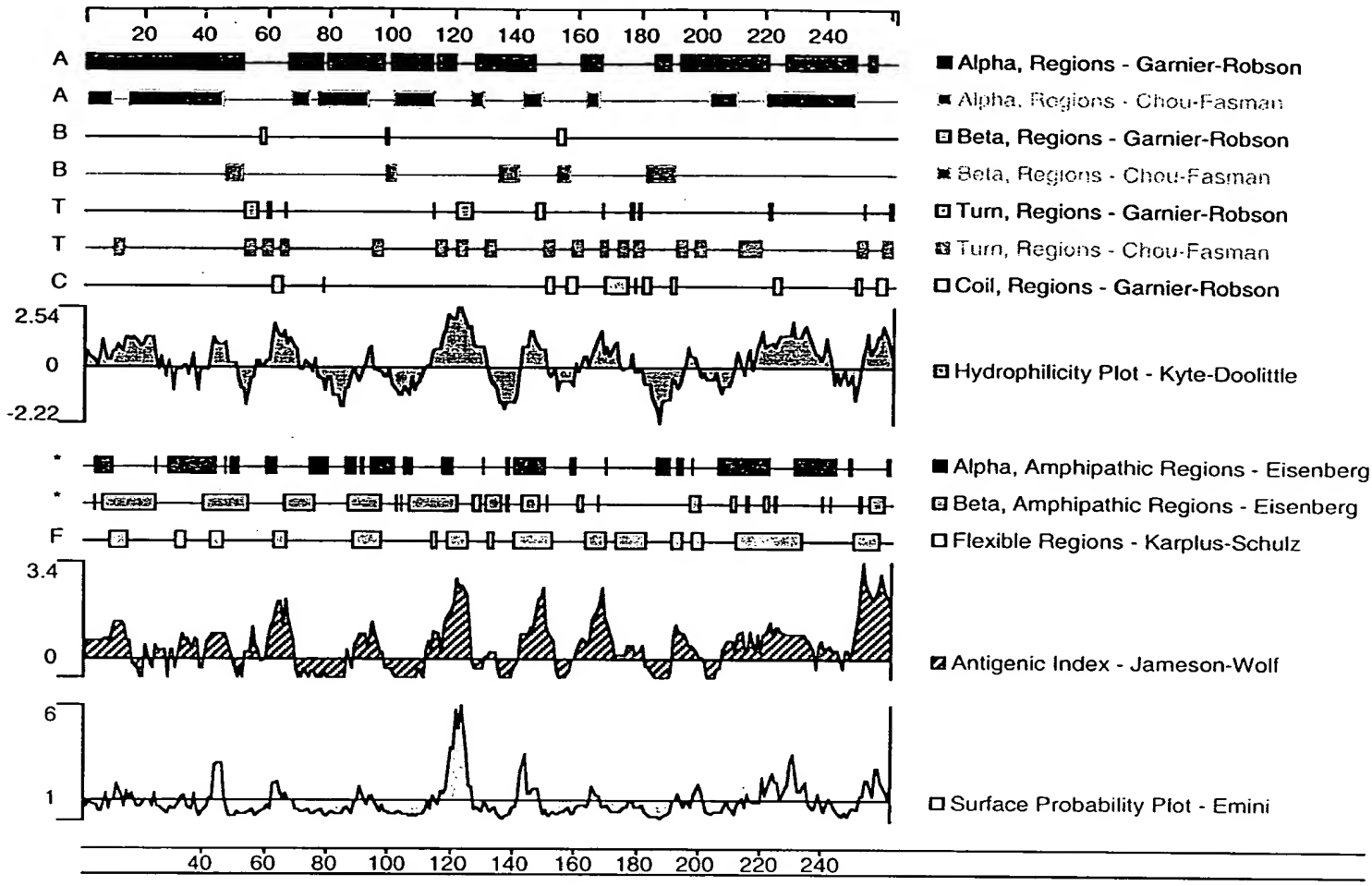
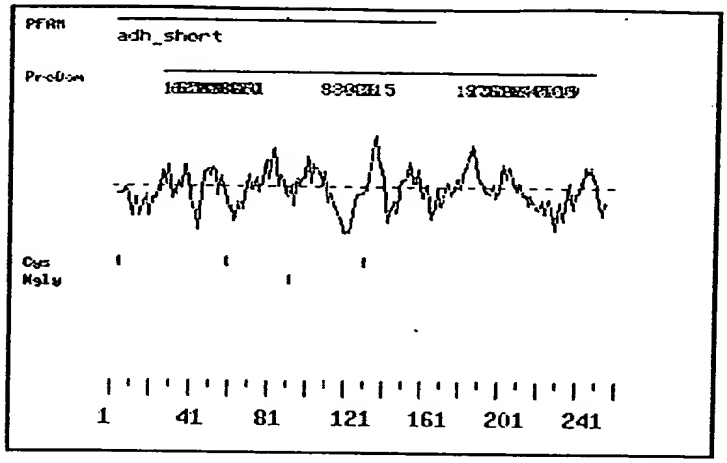

20 40 60 80 100 120 140 160 180 200 220 240
A
A
B
B
T
T
C
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
2.54
0
-2.22
Hydrophilicity Plot - Kyte-Doolittle
*
*
F
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
Flexible Regions - Karplus-Schulz
3.4
0
Antigenic Index - Jameson-Wolf
6
1
Surface Probability Plot - Emini
40 60 80 100 120 140 160 180 200 220 240

FIGURE 8

Back to orfanal.cgi

Analysis of 33756 (260 aa)



Signal Peptide Predictions for 33756

Method	Predict	Score	Mat@
SignalP (eukaryote)	NO		

Note: amino-terminal 70aa used for signal peptide prediction

No TM domains predicted by MEMSAT for 33756

FIGURE 9

Prosite Pattern Matches for 3[redacted]

>PS00001|PDOC00001|ASN_GLYCOSYLATION N-glycosylation site.

Query: 100 NLSS 103

>PS00005|PDOC00005|PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 29 SLK 31

Query: 32 SIR 34

Query: 120 TRK 122

Query: 144 SRR 146

Query: 213 SGK 215

Query: 242 SAR 244

Query: 252 SVR 254

>PS00006|PDOC00006|CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

1

Query: 32 SIRE 35

Query: 63 TTED 66

Query: 252 SVRE 255

>PS00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 149 GSGVTV 154

Query: 160 GVARTE 165

Query: 171 GIHGST 176

FIGURE 10

Input file Fbh21676.seq; Output File 21676.trans
Sequence length 1699

GCNTGTGGGTCCCTTCTTNAAATTGGGTCCCCCCGTTTTAGGTAAGTTTAAAAGCTCAAGGTTCAAAGACNGGNCCTTT

TGTCGGGGGCTCCTTGAAGCCTACTAGATCANCGGCTCTCAGCTTTTTTTTTGGGGGNCCCCCCCCTTTGGGAACCCC

CNTGGCTTTGCTTCAAACTTCTAAGGTCTTTTGTTTCGTTTTCTGTTCCTGCGCCGTTACAGATCCAAGYTCTGAAAAA

CCAGAAAGTTAACTGGTAAGTTTAGTCTTTTTGTCTTTTATTTCAGGTCCCGGATCCGGTGGTGGTGCAAATCAAAGAA

CTGCTCCTCAGTGGATGTTGCCTTTACTTCTAGGCCTGTACGAAGTGTTACTTCTGCTCTAAAAGCTGCGGAATTCTAA

TACGACTCACTATAGGGAGTCGACCCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCGGAGCTACCCAGGCGGCTG

M S R Y 4
GTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGACGCCTGTCCCCGGCCCGGC ATG AGC CGC TAC 12

L L P L S A L G T V A G A A V L L K D Y 24
CTG CTG CCG CTG TCG GCG CTG GGC ACG GTA GCA GGC GCC GCC GTG CTG CTC AAG GAC TAT 72

V T G G A C P S K A T I P G K T V I V T 44
GTC ACC GGT GGG GCT TGC CCC AGC AAG GCC ACC ATC CCT GGG AAG ACG GTC ATC GTG ACG 132

G A N T G I G K Q T A L E L A R R G G N 64
GGC GCC AAC ACA GGC ATC GGG AAG CAG ACC GCC TTG GAA CTG GCC AGG AGA GGA GGC AAC 192

I I L A C R D M E K C E A A A K D I R G 84
ATC ATC CTG GCC TGC CGA GAC ATG GAG AAG TGT GAG GCG GCA GCA AAG GAC ATC CGC GGG 252

E T L N H H V N A R H L D L A S L K S I 104
GAG ACC CTC AAT CAC CAT GTC AAC GCC CGG CAC CTG GAC TTG GCT TCC CTC AAG TCT ATC 312

R E F A A K I I E E E E R V D I L I N N 124
CGA GAG TTT GCA GCA AAG ATC ATT GAA GAG GAG GAG CGA GTG GAC ATT CTA ATC AAC AAC 372

A G V M R C P H W T T E D G F E M Q F G 144
GCG GGT GTG ATG CGG TGC CCC CAC TGG ACC ACC GAG GAC GGC TTC GAG ATG CAG TTT GGC 432

V N H L G H F L L T N L L L D K L K A S 164
GTT AAC CAC CTG GGT CAC TTT CTC TTG ACA AAC TTG CTG CTG GAC AAG CTG AAA GCC TCA 492

A P S R I I N L S S L A H V A G H I D F 184
GCC CCT TCG CGG ATC ATC AAC CTC TCG TCC CTG GCC CAT GTT GCT GGG CAC ATA GAC TTT 552

D D L N W Q T R K Y N T K A A Y C Q S K 204
GAC GAC TTG AAC TGG CAG ACG AGG AAG TAT AAC ACC AAA GCC GCC TAC TGC CAG AGC AAG 612

L A I V L F T K E L S R R L Q G S G V T 224
CTC GCC ATC GTC CTC TTC ACC AAG GAG CTG AGC CGG CGG CTG CAA GGC TCT GGT GTG ACT 672

V N A L H P G V A R T E L G R H T G I H 244
GTC AAC GCC CTG CAC CCC GGC GTG GCC AGG ACA GAG CTG GGC AGA CAC ACG GGC ATC CAT 732

G S T F S S T T L G P I F W L L V K S P 264
GGC TCC ACC TTC TCC AGC ACC ACA CTC GGG CCC ATC TTC TGG CTG CTG GTC AAG AGC CCC 792

E L V A Q P S T Y L A V A E E L A D V S 284
GAG CTG GTC GCC CAG CCC AGC ACA TAC CTG GCC GTG GCG GAG GAA CTG GCG GAT GTT TCC 852

G K Y F D G L K Q K A P A P E A E D E E 304

FIGURE 11

```
GGA AAG TAC TTC GAT GGA CTC AAA CAG AAG GCC CCG GCC CCC GAG GCT GAG GAT GAG GAG  912

 V   A   R   R   L   W   A   E   S   A   R   L   V   G   L   E   A   P   S   V   324
GTG GCC CGG AGG CTT TGG GCT GAA AGT GCC CGC CTG GTG GGC TTA GAG GCT CCC TCT GTG  972

 R   E   Q   P   L   P   R   *                                                   332
AGG GAG CAG CCC CTC CCC AGA TAA                                                  996

CCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAGACCGAGGACAGCTGTCCGCCATGCCCCGCAGCTTCCTGGCA

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TGAAACAT
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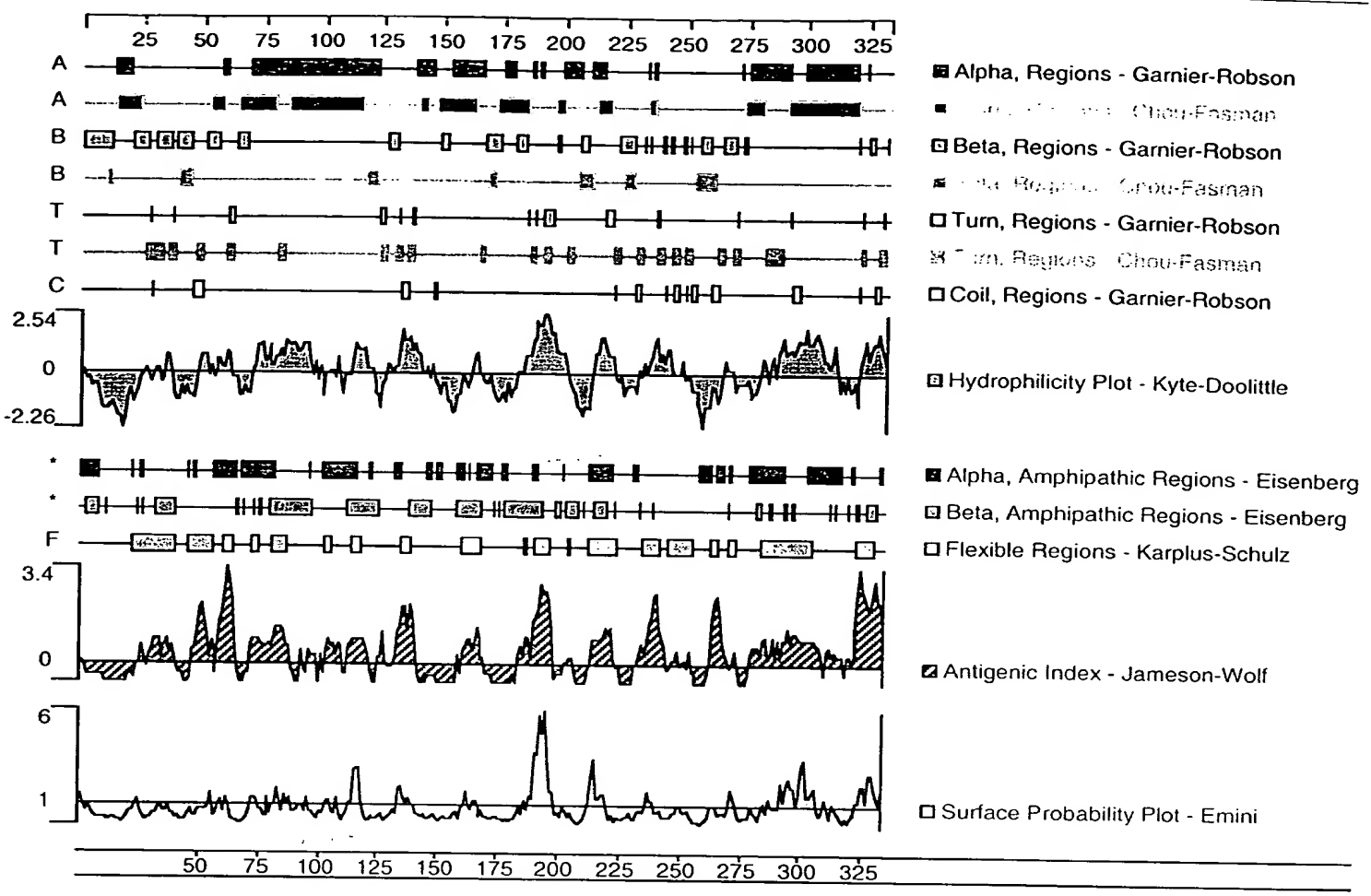
FIGURE 11, Page 2


25 50 75 100 125 150 175 200 225 250 275 300 325
A
A
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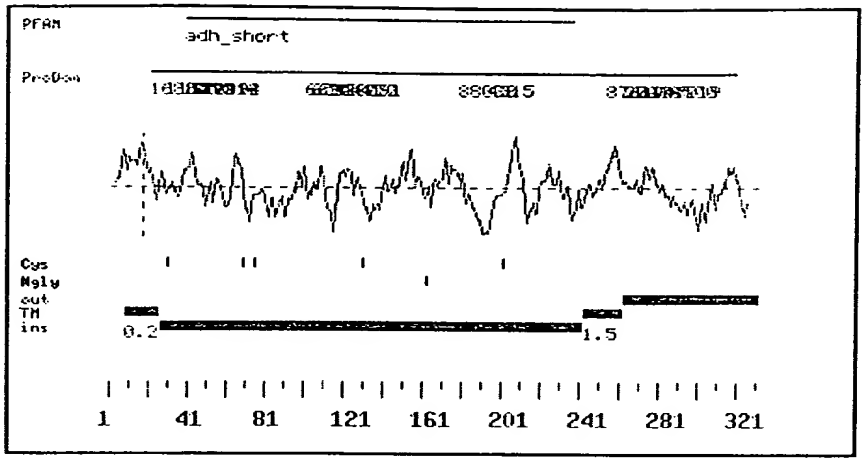
T
C
Alpha, Regions - Garnier-Robson
Beta, Regions - Garnier-Robson
Turn, Regions - Garnier-Robson
Coil, Regions - Garnier-Robson
2.54
0
-2.26
Hydrophilicity Plot - Kyte-Doolittle
*
*
F
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
Flexible Regions - Karplus-Schulz
3.4
0
Antigenic Index - Jameson-Wolf
6
1
Surface Probability Plot - Emini
50 75 100 125 150 175 200 225 250 275 300 325

FIGURE 12

Back to orfanal.cgi

Analysis of 21676 (331 aa)



Signal Peptide Predictions for 21676

Method	Predict	Score	Mat@
SignalP (eukaryote)	YES		17

Note: amino-terminal 70aa used for signal peptide prediction

Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
8	25	out-->ins	0.2
242	261	ins-->out	1.5

Transmembrane segments for presumed mature peptide

Start	End	Orient	Score
226	245	out-->ins	2.1

FIGURE 13

Prosite Pattern Matches for 21676

>PS00001|PDOC00001|ASN_GLYCOSYLATION N-glycosylation site.

Query: 171 NLSS 174

>PS00005|PDOC00005|PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 100 SLK 102
Query: 103 SIR 105
Query: 191 TRK 193
Query: 215 SRR 217
Query: 284 SGK 286
Query: 313 SAR 315
Query: 323 SVR 325

>PS00006|PDOC00006|CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 54 TALE 57
Query: 103 SIRE 106
Query: 134 TTED 137
Query: 323 SVRE 326

>PS00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 12 GTVAGA 17
Query: 28 GACPSK 33
Query: 45 GANTGI 50
Query: 220 GSGVTV 225
Query: 231 GVARTE 236
Query: 242 GIHGST 247

FIGURE 14

Input file Fbh21612f11.seq; Output File 21612.trans
Sequence length 2535

AGGCAGAAGTATGCAAAGCATGCATCTCAAATTAGTCAGCAAACCATAGTCCCGGCCCCTAACTCCGCCCATCCCGCCC

CTAACTCCGNCCCAGTTCCGGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGCCGAGGCCGCC

TCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTCCTCGATCGAG

GGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCTACCTGAGGCCGCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCC

TCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCG

GCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTACGTCTTTG

TTTCAGTTTTCTGTTCTGCGCCGTTACAGATCCAAGCTCTGAAAAACCAGAAAGTTAACTGGTAAGTTTAGTCTTTTTG

TCTTTTATTTCAGGTCCCGGATCCGGTGGTGGTGCAAATCAAAGAACTGCTCCTCAGTGGATGTTGCCTTTACTTCTAG

GCCTGTACGGAAGTGTTACTTCTGCTCTAAAAGCTGCGGAATTCTAATACGACTCACTATAGGGWGTCGACCCACGCGT

M L P N T G R 7
CCGCTCGCCGCCGCCGCTGTCGCCGCCACCTCCTCTGATCTACGAAAGTC ATG TTA CCC AAC ACC GGG AGG 21

L A G C T V F I T G A S R G I G K A I A 27
CTG GCA GGA TGT ACA GTT TTT ATC ACA GGT GCA AGC CGT GGC ATT GGC AAA GCT ATT GCA 81

L K A A K D G A N I V I A A K T A Q P H 47
TTG AAA GCA GCA AAG GAT GGA GCA AAT ATT GTT ATT GCT GCA AAG ACC GCC CAG CCA CAT 141

P K L L G T I Y T A A E E I E A V G G K 67
CCA AAA CTT CTA GGC ACA ATC TAT ACT GCT GCT GAA GAA ATT GAA GCA GTT GGA GGA AAG 201

A L P C I V D V R D E Q Q I S A A V E K 87
GCC TTG CCA TGT ATT GTT GAT GTG AGA GAT GAA CAG CAG ATC AGT GCT GCA GTG GAG AAA 261

A I K K F G G I D I L V N N A S A I S L 107
GCC ATC AAG AAA TTT GGA GGA ATT GAT ATT CTG GTA AAT AAT GCC AGT GCC ATT AGT TTG 321

T N T L D T P T K R L D L M M N V N T R 127
ACC AAT ACA TTG GAC ACA CCT ACC AAG AGA TTG GAT CTG ATG ATG AAC GTG AAC ACC AGA 381

G T Y L A S K A C I P Y L K K S K V A H 147
GGC ACC TAC CTT GCA TCT AAA GCA TGT ATT CCT TAT TTG AAA AAG AGC AAA GTT GCT CAT 441

I L N I S P P L N L N P V W F K Q H C A 167
ATC CTC AAT ATC AGT CCA CCA CTG AAC CTA AAT CCA GTT TGG TTC AAA CAG CAC TGT GCT 501

Y T I A K Y G M S M Y V L G M A E E F K 187
TAT ACC ATT GCT AAG TAT GGT ATG TCT ATG TAT GTG CTT GGA ATG GCA GAA GAA TTT AAA 561

G E I A V N A L W P K T A I H T A A M D 207
GGT GAA ATT GCA GTC AAT GCA TTA TGG CCT AAA ACA GCC ATA CAC ACT GCT GCT ATG GAT 621

M L G G P G I E S Q C R K V D I I A D A 227
ATG CTG GGA GGA CCT GGT ATC GAA AGC CAG TGT AGA AAA GTT GAT ATC ATT GCA GAT GCA 681

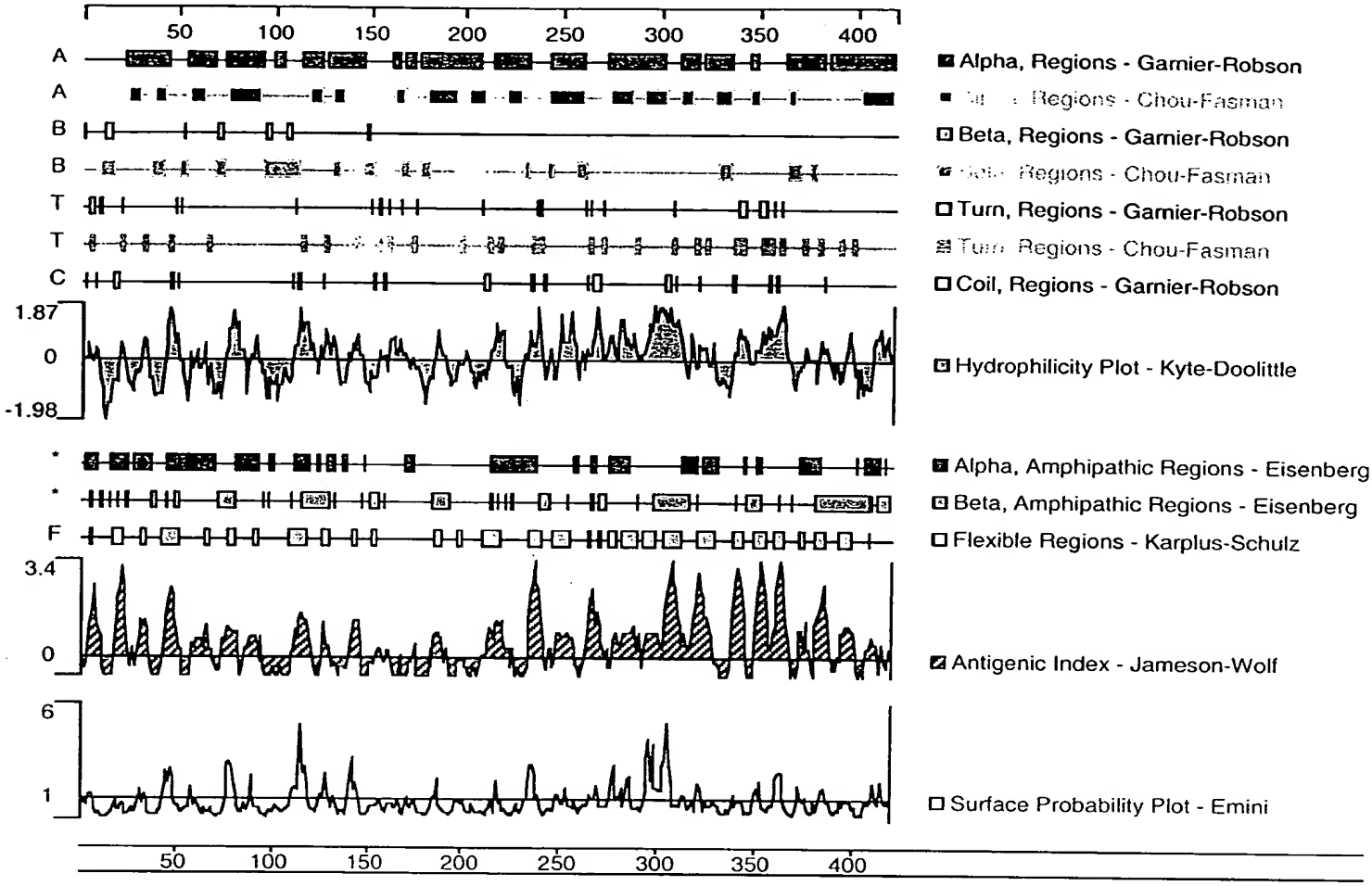
A Y S I F Q K P K S F T G N F V I D E N 247
GCA TAT TCC ATT TTC CAA AAG CCA AAA AGT TTT ACT GGC AAC TTT GTC ATT GAT GAA AAT 741

I L K E E G I E N F D V Y A I K P G H P 267

FIGURE 15

```
ATC TTA AAA GAA GAA GGA ATA GAA AAT TTT GAC GTT TAT GCA ATT AAA CCA GGT CAT CCT   801

 L  Q  P  D  F  F  L  D  E  Y  P  E  A  V  S  K  K  V  E  S                    287
TTG CAA CCA GAT TTC TTC TTA GAT GAA TAC CCA GAA GCA GTT AGC AAG AAA GTG GAA TCA   861

 T  G  A  V  P  E  F  K  E  E  K  L  Q  L  Q  P  K  P  R  S                    307
ACT GGT GCT GTT CCA GAA TTC AAA GAA GAG AAA CTG CAG CTG CAA CCA AAA CCA CGT TCT   921

 G  A  V  E  E  T  F  R  I  V  K  D  S  L  S  D  D  V  V  K                    327
GGA GCT GTG GAA GAA ACA TTT AGA ATT GTT AAG GAC TCT CTC AGT GAT GAT GTT GTT AAA   981

 A  T  Q  A  I  Y  L  F  E  L  S  G  E  D  G  G  T  W  F  L                    347
GCC ACT CAA GCA ATC TAT CTG TTT GAA CTC TCC GGT GAA GAT GGT GGC ACG TGG TTT CTT  1041

 D  L  K  S  K  G  G  N  V  G  Y  G  E  P  S  D  Q  A  D  V                    367
GAT CTG AAA AGC AAG GGT GGG AAT GTC GGA TAT GGA GAG CCT TCT GAT CAG GCA GAT GTG  1101

 V  M  S  M  T  T  D  D  F  V  K  M  F  S  G  K  L  K  P  T                    387
GTG ATG AGT ATG ACT ACT GAT GAC TTT GTA AAA ATG TTT TCA GGG AAA CTA AAA CCA ACA  1161

 M  A  F  M  S  G  K  L  K  I  K  G  N  M  A  L  A  I  K  L                    407
ATG GCA TTC ATG TCA GGG AAA TTG AAG ATT AAA GGT AAC ATG GCC CTA GCA ATC AAA TTG  1221

 E  K  L  M  N  Q  M  N  A  R  L  *                                            419
GAG AAG CTA ATG AAT CAG ATG AAT GCC AGA CTG TGA                                 1257

AGGAAAATATAAAAAAAAAGTCGACTGCTATGCTCAAAAAGTAAAAAAAGCTCAACAGTTAAAATCTAATGTTTGTTTT

CTTTCCTGTTATATTATAAGGATATGCACGTTTGTTCTGGAAAAGATAGAATTTGTCTCTAAAAGACTTGAAATTGTAA

TTAAAATGGCAAGCTAATCAAACATAAGCTTCATTAAGTGGGATTCTAAGACAGTCTGTGTTTTTATATTTCAAGGGTT

TAACCCTTTGAGCCTTACATCTCATTCACTGTCTTTCTCCAAGAAAAGTATTTTGGGCGGACAGTCAGATCAAGCAGTA

AAATTAGCTCTTTCAAATCTTCTTGTCATGTAAAATGAAGCTAGTCTGTTTTAAAATTTTTAGTTTTGGATTGTATACT

AATGAAAATCTTAATGATGTTTTKRWTTTTTATATACYTAWTTTWAARRAAAWYYTWWWWWRKWCMTTTTWMCAAAAAW

TWTTAAAAAWKRRWWWKWRYTSKGSGMGRASWMWAWRWRAMMC
```

FIGURE 15, Page 2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100
150
200
250
300
350
400
A
A
B
B
T
T
C
Alpha, Regions - Garnier-Robson
Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
1.87
0
-1.98
Hydrophilicity Plot - Kyte-Doolittle
*
*
F
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
Flexible Regions - Karplus-Schulz
3.4
0
Antigenic Index - Jameson-Wolf
6
1
Surface Probability Plot - Emini
50
100
150
200
250
300
350
400

FIGURE 16

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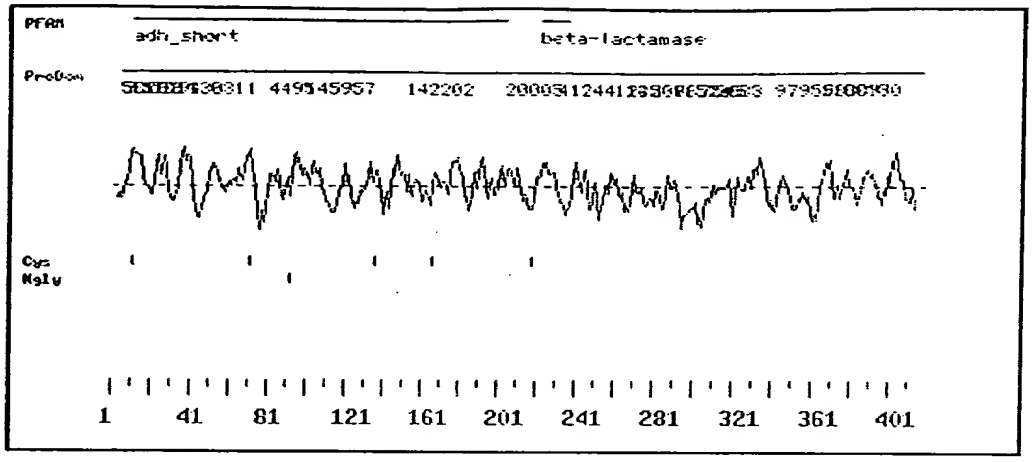
Analysis of 21612 (418 aa)



Signal Peptide Predictions for 21612

Method	Predict	Score	Mat@
SignalP (eukaryote)	NO		

Note: amino-terminal 70aa used for signal peptide prediction

No TM domains predicted by MEMSAT for 21612

FIGURE 17

Prosite Pattern Mat[redacted] for 21612

>PS00001|PDOC00001|ASN_GLYCOSYLATION N-glycosylation site.

Query: 101 NASA 104

>PS00005|PDOC00005|PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 5 TGR 7

Query: 115 TKR 117

Query: 282 SKK 284

Query: 313 TFR 315

Query: 381 SGK 383

Query: 392 SGK 394

>PS00006|PDOC00006|CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 56 TAAE 59

Query: 320 SLSD 323

Query: 338 SGED 341

Query: 372 TTDD 375

>PS00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 17 GASRGI 22

Query: 52 GTIYTA 57

Query: 128 GTYLAS 133

Query: 353 GGNVGY 358

>PS00342|PDOC00299|MICROBODIES_CTER Microbodies C-terminal targeting signal.

Query: 416 ARL 418

FIGURE 18

> **Fbh21615a - Import - complete**

```
1       ATGCAAAAGC CGAGNCCGCC TCGGCCTCTA AGCTATTCCA GAAGTAGTAA GAAGGCTTTT
61      TTGAAGGCCT AGGCTTTTGC AAAAAGCTCC TCGATCGAGG GGCTCGCATC TCTCCTTCAC
121     GGGGCCGCCG CCCTACCTGA GGCCGCCATC CACGCCGGTT GAGTCGCGTT CTGCCGCCTC
181     CCGCCTGTGG TGCCTCCTGA ACTGCGTCCG CCGTYTAGGT AAGTTTAAAG CTCAGGTCGA
241     GACCGGGCCT TTGTCCGGCG CTCCCTTGGA GCCTACCTAG ACTCAGCCGG CTCTCCACGC
301     TTTGCCTGAC CCTGCTTGCT CAACTCTACG TCTTTGTTTC GTTTTCTGTT CTGCGCCGTT
361     ACAGATCCAA GCTCTGAAAA ACCAGAAAGT TAACTGGTAA GTTTAGTCTT TTTGTCTTTT
421     ATTTCAGGTC CCGGATCCGG TGGTGGTGCA AATCAAAGAA CTGCTCCTCA GTGGATGTTG
481     CCTTTACTTC TAGGCCTGTA CGGAAGTGTT ACTTCTGCTC TAAAAGCTGC GGAATTCTAA
541     TACGACTCAC TATAGGGAGT CGACCCACGC GTCCGCAAAC CGAGTTCTGG AGAACGCCAT
601     CAGCTCGCTG CTTAAAATTA AACCACAGGT TCCATTATGG GTCGACTTGA TGGGAAAGTC
661     ATCATCCTGA CGGCCGCTGC TCAGGGGATT GGCCAAGCAG CTGCCTTAGC TTTTGCAAGA
721     GAAGGTGCCA AAGTCATAGC CACAGACATT AATGAGTCCA AACTTCAGGA ACTGGAAAAG
781     TACCCGGGTA TTCAAACTCG TGTCCTTGAT GTCACAAAGA AGAAACAAAT TGATCAGTTT
841     GCCAATGAAG TTGAGAGACT TGATGTTCTC TTTAATGTTG CTGGTTTTGT CCATCATGGA
901     ACTGTCCTGG ATTGTGAGGA GAAAGACTGG GACTTCTCGA TGAATCTCAA TGTGCGCAGC
961     ATGTACCTGA TGATCAAGGC ATTCCTTCCT AAAATGCTTG CTCAGAAATC TGGCAATATT
1021    ATCAACATGT CTTCTGTGGC TTCCAGCGTC AAAGGAGTTG TGAACAGATG TGTGTACAGC
1081    ACAACCAAGG CAGCCGTGAT TGGCCTCACA AAATCTGTGG CTGCAGATTT CATCCAGCAG
1141    GGCATCAGGT GCAACTGTGT GTGCCCAGGA ACAGTTGATA CGCCATCTCT ACAAGAAAGA
1201    ATACAAGCCA GAGGAAATCC TGAAGAGGCA CGGAATGATT TCCTGAAGAG ACAAAAGACG
1261    GGAAGATTCG CAACTGCAGA AGAAATAGCC ATGCTCTGCG TGTATTTGGC TTCTGATGAA
1321    TCTGCTTATG TAACTGGTAA CCCTGTCATC ATTGATGGAG GCTGGAGCTT GTGATTTTAG
1381    GATCTCCATG GTGGGAAGGA AGGCAGGCCC TTCCTATCCA CAGTGAACCT GGTTACGAAG
1441    AAAACTCACC AATCATCTCC TTCCTGTTAA TCACATGTTA ATGAAAATAA GCTCTTTTTA
1501    ATGATGTCAC TGTTTGCAAG AGTCTGATTC TTTAAGTATA TTAATCTCTT TGTAATCTCT
1561    TCTGAAATCA TTGTAAAGAA ATAAAAATAT TGAACTCAAA AAAAAAAAAA AAAAAAGGGC
1621    GGCCGCTAGA CTAGTCTAGA GAAAAAACCT CCCACACCTC CCCCTGAACC TGAAACATAA
1681    AATGAATGCM ATTGTTGKTG GTAACTTGTT ATTGCA
```

FIGURE 19A

> Fbh21615a - Import - complete

MGRWDGKV IILTAAAQGI GQAAALAFAR
EGAKVIATDI NESKLQELEK YPGIQTRVLD VTKKKQIDQF ANEVERLDVL FNVAGFVHHG
TVLDCEEKDW DFSMNLNVRS MYLMIKAFLP KMLAQKSGNI INMSSVASSV KGVVNRCVYS
TTKAAVIGLT KSVAADFIQQ GIRCNCVCPG TVDTPSLQER IQARGNPEEA RNDFLKRQKT
GRFATAEEIA MLCVYLASDE SAYVTGNPVI IDGGWSL*

FIGURE 19B

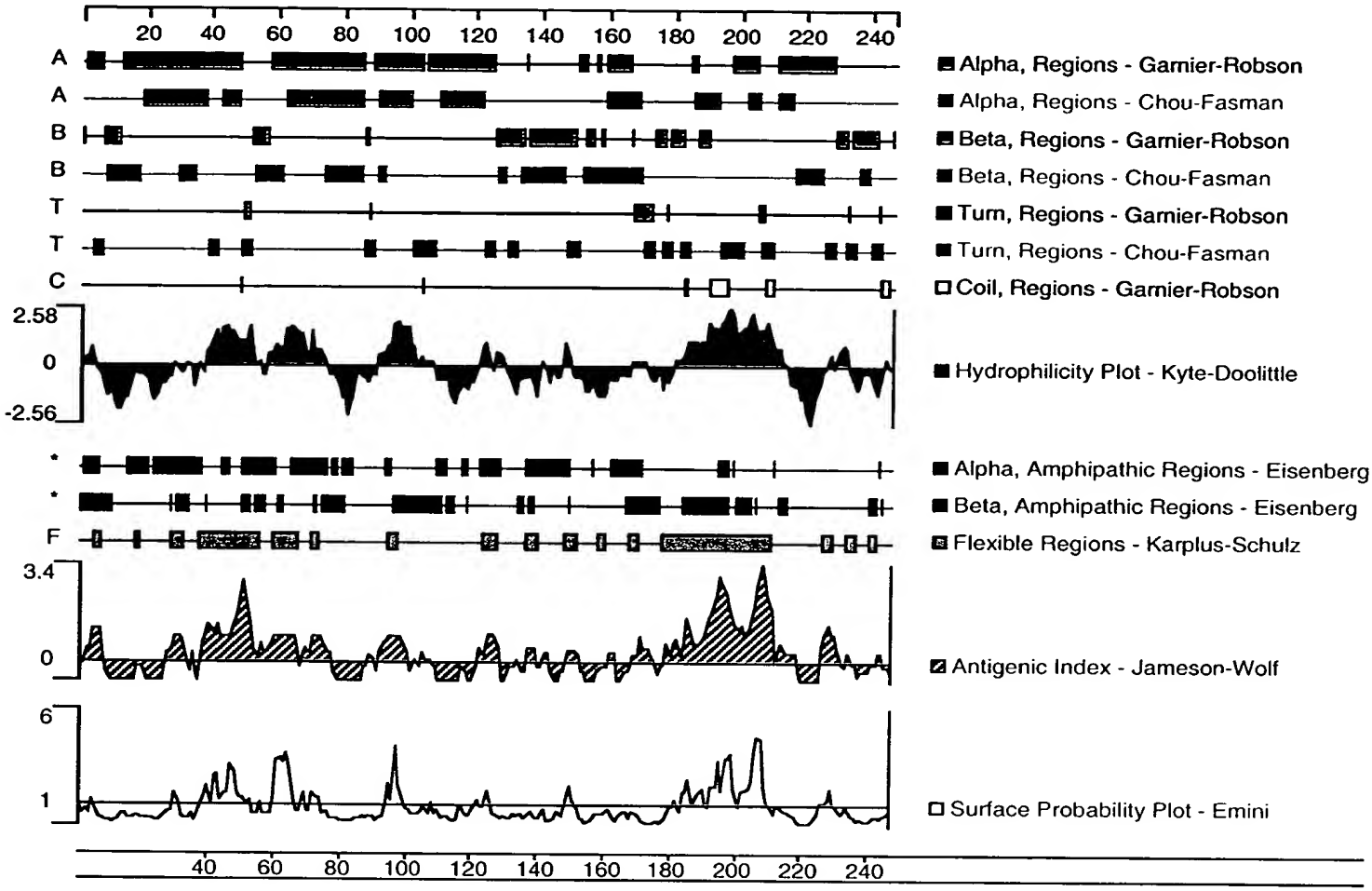

20 40 60 80 100 120 140 160 180 200 220 240
A
A
B
B
T
T
C
2.58
0
-2.56
*
*
F
3.4
0
6
1
40 60 80 100 120 140 160 180 200 220 240
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
Hydrophilicity Plot - Kyte-Doolittle
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
Flexible Regions - Karplus-Schulz
Antigenic Index - Jameson-Wolf
Surface Probability Plot - Emini

FIGURE 20

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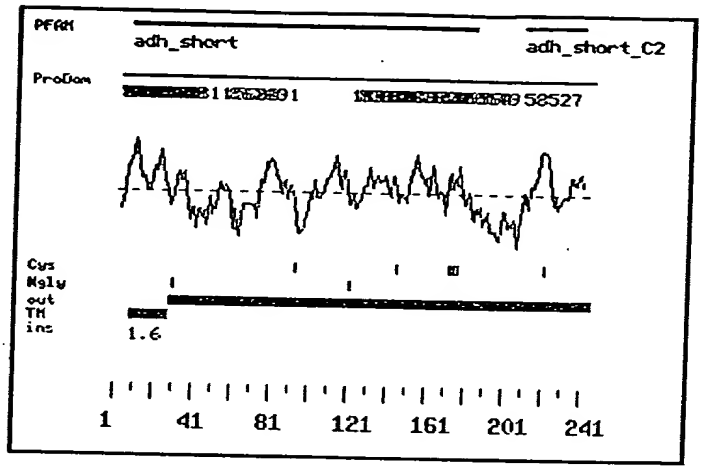
Analysis of 21615 (245 aa)



Signal Peptide Predictions for 21615

Method	Predict	Score	Mat@
SignalP (eukaryote)	NO		

Note: amino-terminal 70aa used for signal peptide prediction

Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
8	27	ins-->out	1.6

FIGURE 21

Prosite Pattern Matches for 21615

>PS00001|PDOC00001|ASN_GLYCOSYLATION N-glycosylation site.

Query: 39 NESK 42

Query: 130 NMSS 133

>PS00005|PDOC00005|PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 60 TKK 62

Query: 137 SVK 139

Query: 149 TTK 151

Query: 208 TGR 210

>PS00006|PDOC00006|CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 89 TVLD 92

Query: 184 SLQE 187

Query: 213 TAEE 216

>PS00007|PDOC00007|TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.

Query: 42 KLQELEKY 49

>PS00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 17 GIGQAA 22

Query: 126 GNIINM 131

Query: 156 GLTKSV 161

Query: 169 GIRCNC 174

>PS00061|PDOC00060|ADH_SHORT Short-chain alcohol dehydrogenase family signature.

Query: 147 YSTTKAAVIGL 157

FIGURE 22